Figure 1

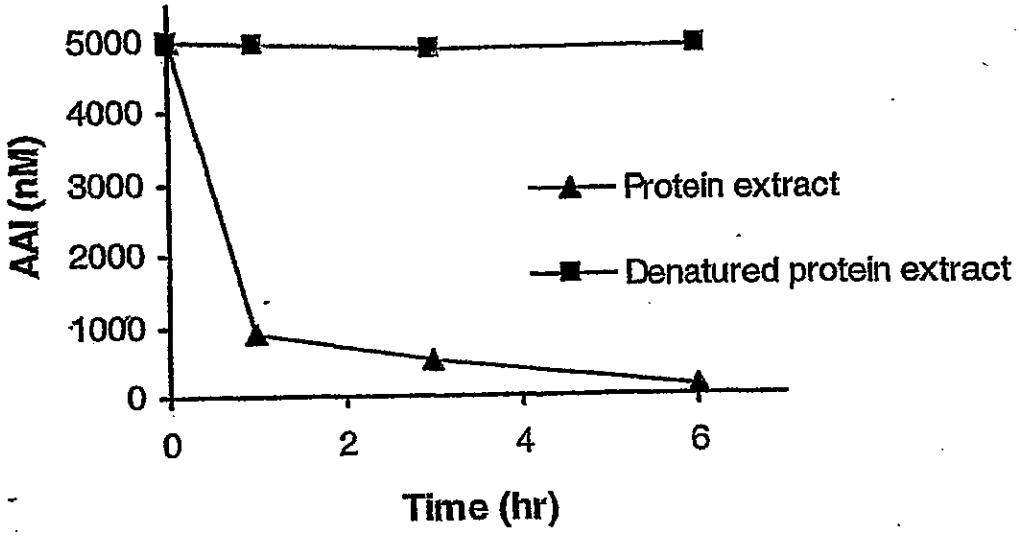

5000
4000
3000
2000
1000
0
AAI (nM)
0
2
4
6
Time (hr)
Protein extract
Denatured protein extract

Figure 2

Clones	Activity
cosmid clone 1	+
cosmid clone 4	+
sub-clone 1	-
sub-clone 2	+
sub-clone 3	-
sub-clone 4	+

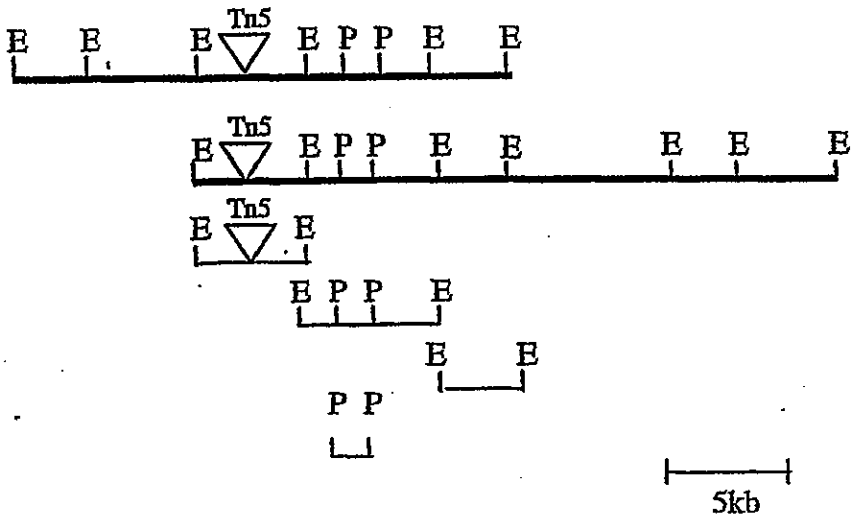
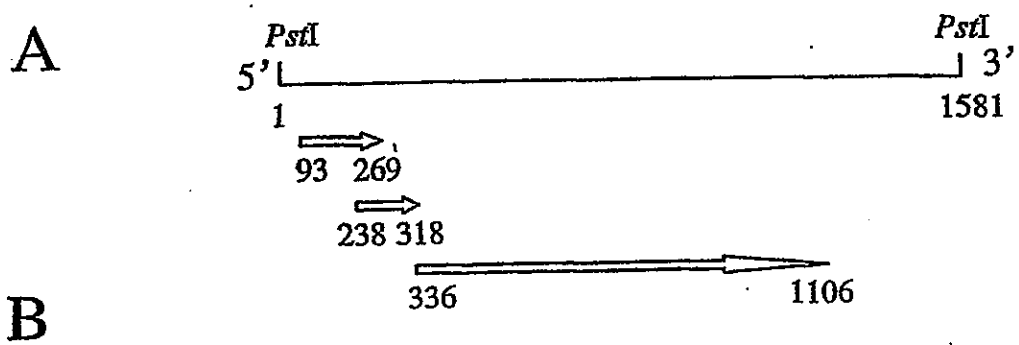


Figure 3



B

Clones	Activity
pBM103-160	+
pBM103-280	+
pBM103-230	+
pBM103-296	+
pKM103-310	+
pKM103-320	-
pKM103-330	-
pKM103-336	-
pKM103-315	+

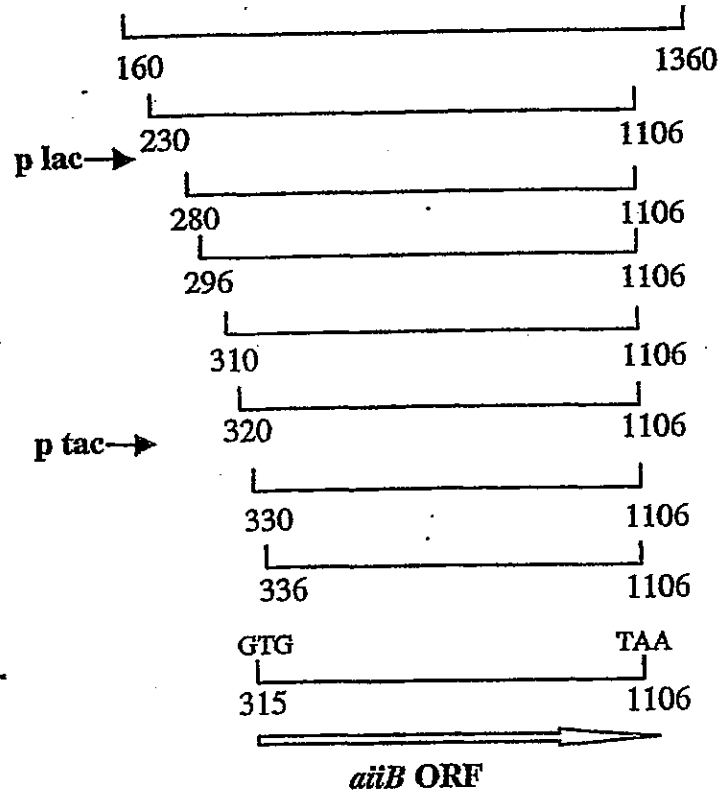


Figure 4

A

```
                                                    PstI
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GATGCGTTCGTTCAGCATATGGAAACGCTGATGGACGAAAGCGGCGCGCCGCGACGTCTG -180
CGCGATGTCGGCGTGACGGACAACACGCTCGCCATGCTTGCGTCCGACGCAATGAAACAG -120
AGCCGTCTGTTGGTCAATAATCCGGTCGAAGTCCGCGAAGAGGATGCGCTTGCGCTCTAC -60
CGCGAGGCGTTCTGACCCATTTCTGACAGCAATATCTTCAGTCCCAAGGGAGGAAAACGA -1
                                                      SD
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start
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ACCCATCCGGGCGGGCACACCGTGATCGACGGCGGCAACGCGATTGAAGTTGCAACGGAT 180
CCGCGTGGCCATTGGGGCGGCATCTGCGATGTCTATTGGCCAGTGCTGGACAAGGACCAG 240
GGCTGCGTTGACCAGATCAAGGCGCTTGGTTTCGATCCGGCCGATGTCAAGTATGTTGTG 300
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GCGACGGTCGTTACCGGCCATGACCCTGACGCGTGGGCGAACTTCAAGAAGGCTCCCGAA 780
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      stop
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GCAGAGGCCTTTTCAGGATATACGCCTTCACTCAGGTCGTTCGCGTTGTCGCCTCAAGGC 960
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TGAAACCCGCGCCGGCCAGCAATGAAACGACCTCGTCTTCCGATCGGGGTGGCTCTGCAC 1260
CCTGCAG                                                        1267
PstI
```

B

```
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GCVDQIKALGFDPADVKYVVQSHLHLDHTGAIGRFPNATH 120
IVQRSEYEYAFTPDWFAGGGYIRKDFDKPGLKWQFLNGTQ 160
DDYYDVYGDGTLTTIFTPGHAPGHQSLLVRLPNSKPLLLT 200
IDAAYTLDHWEEKALPGFLASTVDTVRSVQKLRTYAEKHD 240
ATVVTGHDPDAWANFKKAPEFYA.                  263
```

Figure 5

```
AiiB : 1                                                        VTDIRLY  7

AttM                                                            -------

AiiB : 8    MLQSGTLKCKVHNIKMNQGNGADYEIPVPFFLITHPGGHTVIDGGNAIEVATDPRGHWGG 67
            MLQSGTLKCKVHNIKMNQGNGADYEIPVPFFLITHP GHTVIDGGNAIEVATDPRGHWGG
AttM : 1    MLQSGTLKCKVHNIKMNQGNGADYEIPVPFFLITHPAGHTVIDGGNAIEVATDPRGHWGG 60

AiiB : 68   ICDVYWPVLDKDQGCVDQIKALGFDPADVKYVVQSHLHLDHTGAIGRFPNATHIVQRSEY 127
            ICDVYWPVLDKDQGCVDQIKALGFDPADVKYVVQSHLHLDHTGAIGRFPNATHIVQRSEY
AttM : 61   ICDVYWPVLDKDQGCVDQIKALGFDPADVKYVVQSHLHLDHTGAIGRFPNATHIVQRSEY 120

AiiB : 128  EYAFTPDWFAGGGYIRKDFDKPGLKWQFLNGTQDDYYDVYGDGTLTTIFTPGHAPGHQSL 187
            EYAFTPDWFAGGGYIRKDFDKPGLKWQFLNG QDDYYDVYGDGTLTTIFTPGHAPGHQS
AttM : 121  EYAFTPDWFAGGGYIRKDFDKPGLKWQFLNGAQDDYYDVYGDGTLTTIFTPGHAPGHQSF 180

AiiB : 188  LVRLPNSKPLLLTIDAAYTLDHWEEKALPGFLASTVDTVRSVQKLRTYAEKHDATVVTGH 247
            LVRLPNSKPLLLTIDAAYTLDHWEEKALPGFLASTVDTVRSVQKLRTYAEKHDATVVTGH
AttM : 181  LVRLPNSKPLLLTIDAAYTLDHWEEKALPGFLASTVDTVRSVQKLRTYAEKHDATVVTGH 240

AiiB : 248  DPDAWANFKKAPEFYA 263
            DPDAWANFKKAPEFYA
AttM : 241  DPDAWANFKKAPEFYA 256
```

Figure 6

```
   .T...LY....G...C.......N.......  Consensus

1  VTDIRLYMLQSGTLKCKVHNIKMNQGNGAD  AiiB protein.PRO
1  MTVKKLYFVPAG--RCMLDHSSVNSTLTPG  AiiA protein.PRO

   .....P....L.....G....D.G...E.A  Consensus

31 YEIPVPF--FLITHPGGHTVIDGGNAIEVA  AiiB protein.PRO
29 ELLDLPVWCYLLETEEGPILVDTGMP-ESA  AiiA protein.PRO

   ....G...G......V..P.........V..  Consensus

59 TDPRGHWGGI---CDVYWPVLDKDQGCVDQ  AiiB protein.PRO
58 VNNEGLFNGTFVEGQVL-PKMTEEDRIVNI  AiiA protein.PRO

   .K..G..P.D..Y...SHLH.DH.G..G.F  Consensus

86 IKALGFDPADVKYVVQSHLHLDHTGAIGRF  AiiB protein.PRO
87 LKRVGYEPEDLLYIISSHLHFDHAGGNGAF  AiiA protein.PRO

   .N...IVQR.EYE............Y..K.  Consensus

116 PNATHIVQRSEYEYAFTPDWFAGGGYIRKD  AiiB protein.PRO
117 INTPIIVQRAEYE---AAQ--HSEEYL-KE  AiiA protein.PRO

   ...P.L......G.....Y.V.....L...  Consensus

146 FDKPGLKWQFLNGTQDDYYDVYGDGTLTTI  AiiB protein.PRO
141 CILPNLNYKIIEGD----YEVVPGVQL--L  AiiA protein.PRO

   .TPGH.PGHQSLL.....S.P.LLTIDA.Y  Consensus

176 FTPGHAPGHQSLLVRLPNSKPLLLTIDAAY  AiiB protein.PRO
165 HTPGHTPGHQSLLIETEKSGPVLLTIDASY  AiiA protein.PRO

   T....E......GF.........S...L..  Consensus

206 TLDHWEEKA-LPGFLASTVDTVRSVQKLRT  AiiB protein.PRO
195 TKENFENEVPFAGFDSEL--ALSSIKRLKE  AiiA protein.PRO

   ...K....V..GHD..............PE  Consensus

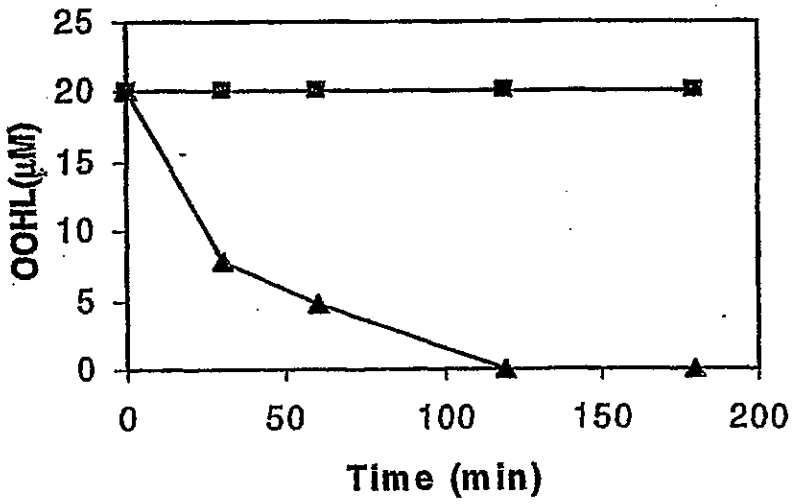
235 YAEKHDATVVTGHDPDAWANFKKA----PE  AiiB protein.PRO
223 VVMKEKPIVFFGHDIEQ----ERGCKVFPE  AiiA protein.PRO

   .Y.-                             Consensus

261 FYA.                           AiiB protein.PRO
249 -YI.                           AiiA protein.PRO
```

Figure 7

A


25
20
15
10
5
0
OOHL(μM)
0
50
100
150
200
Time (min)

B

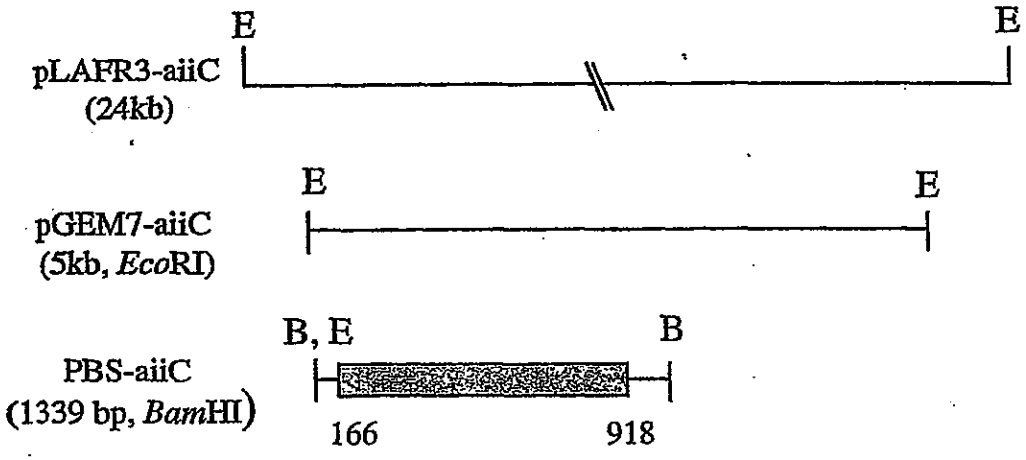

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(24kb)
E
E
pGEM7-aiiC
(5kb, EcoRI)
B, E
B
PBS-aiiC
(1339 bp, BamHI)
166
918

Figure 8

aiiC seq

A

```
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GCGCCGGGAAATTTATTGAACTTACCTGTATGGTGTTATCTTTTGGAGACGGAAGAAGGT    300
CCCATTTTAGTAGATACAGGTATGCCAGAAAGTGCGGTTAATAATGAAAACTTGTTTGAA    360
GGGACATTTGCAGAAGGACAGATTTTACCGAAAATGACTGAAGAAGATAGAATAATAGCT    420
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CATTTTGATCATGCAGGAGGAAATGGTGCTTTTATTAATACTCCAATCATTATACAGCGT    540
GCTGAATATGAGGCAGCGCAGTATAGAGAGGAATATTTGAAAGAGTGTATACTGCCGAAT    600
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GCTGGATTTGATCCAGAATTAGCTTTATCATCAATTAAACGTTTAAAAGAAGTTGTGATG    840
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tcatactgttaatgaatgtctttaattcatctgtttttgcgagaaagatatctttttttg   1260
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catttggatcccttgagt                                             1339
```

B

```
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IIIQRAEYEAAQYREEYLKECILPNLNYKIIEGDYEVVPGVQLLYTPGHSPGHQSLLIET   180
EKSGVVLLTIDASYTKENFEDEVPFAGFDPELALSSIKRLKEVVMKEKPLVFFGHDIEQE   240
KGCKVFPEYI                                                     250
```

Figure 9

aiiD

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Figure 9 (continued)

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aiiH

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aiiI

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KGCRVFPEYI

aiiJ

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aiiK

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Figure 9 (continued)

GATAGAATCGTGAATATATTAAAGCGTGTAGGGTATGAGCCGGACGACCTTTTATATATTATTAGTTCTCACTTACATTT
TGATCATGCAGGAGGAAACGGTGCTTTTACAAATACACCGATTATTGTGCAGCGAACGGAATATGAGGCAGCACTTCATA
GAGAAGAATATATGAAAGAATGTATATTACCGCATTTGAACTACAAAATTATTGAAGGGGATTATGAAGTGGTaCCAGGT
GTTCAATTATTGTATACGCCAGGTCATTCTCCAGGCCATCAGTCGTTATTCATTGAGACGGAGCAATCCGGTTCAGTTTT
ATTAACAATTGATGCATCGTACACGAAAGAGAATTTTGAAGATGAAGTGCCGTTCGCAGGATTTGATCCAGAATTAGCTT
TATCTTCAATTAAACGTTTAAAAGGAGTTGTGGCGAAAGAGAAACCAATTGTTTTCTTTGGTCATGATATAGAGCAGGAA
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MTVKKLYFIPAGRCMLDHSSVNGTLAPGNLLNLPVWCYLLETEEGAILVDTGMPESAVNNEGLFNGTFVEGQILPKMTEE
DRIVNILKRVGYEPDDLLYIISSHLHFDHAGGNGAFTNTPIIVQRTEYEAALHREEYMKECILPHLNYKIIEGDYEVVPG
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Figure 10

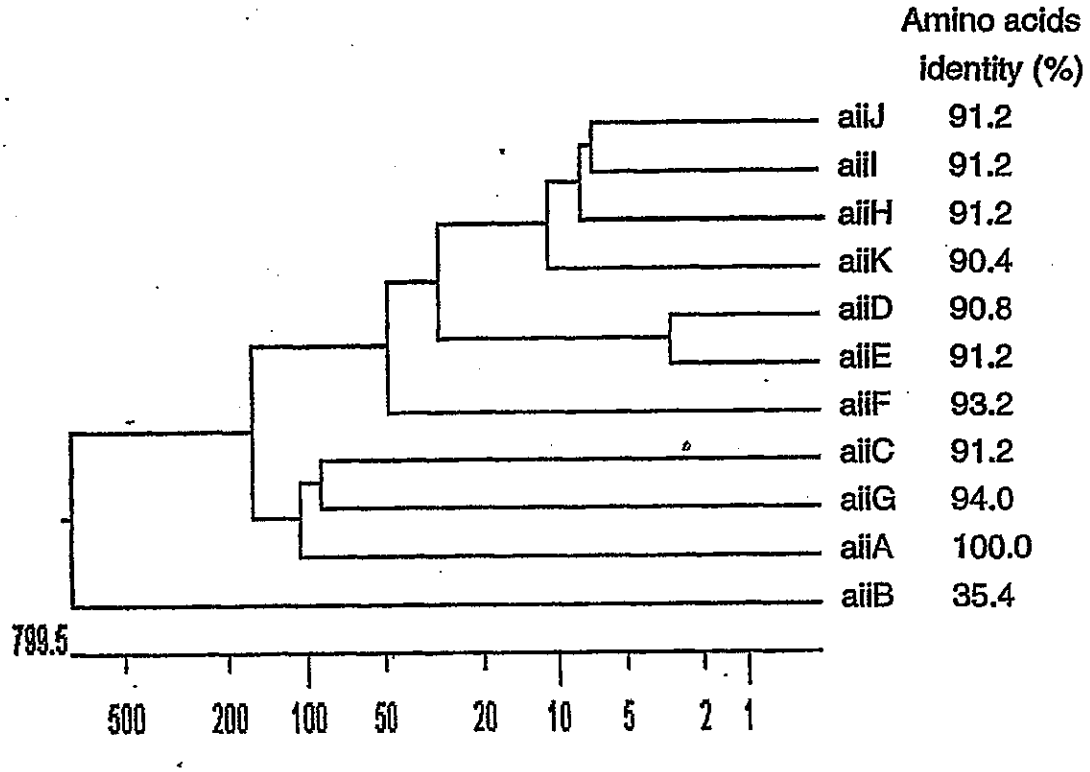

Amino acids identity (%)
aiiJ 91.2
aiiI 91.2
aiiH 91.2
aiiK 90.4
aiiD 90.8
aiiE 91.2
aiiF 93.2
aiiC 91.2
aiiG 94.0
aiiA 100.0
aiiB 35.4
799.5
500 200 100 50 20 10 5 2 1

Figure 11

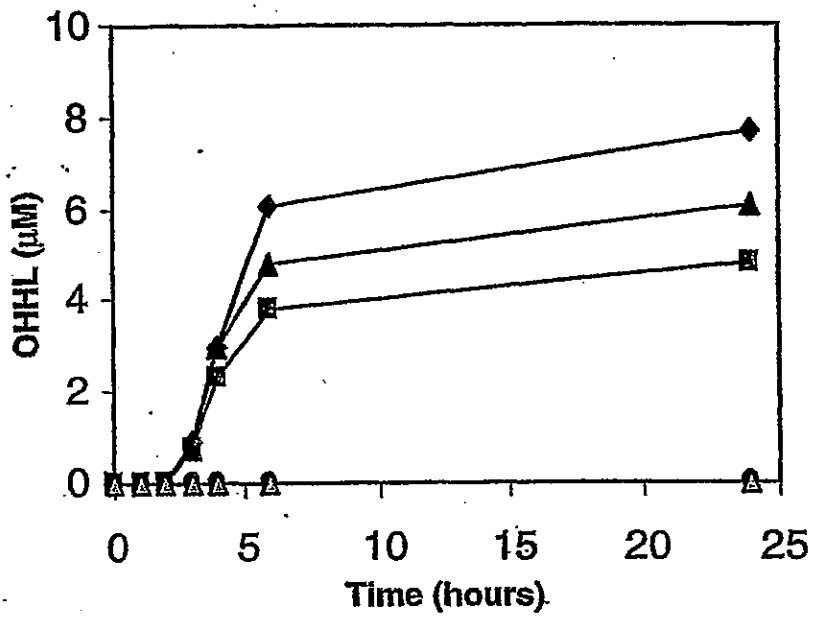


Figure 12

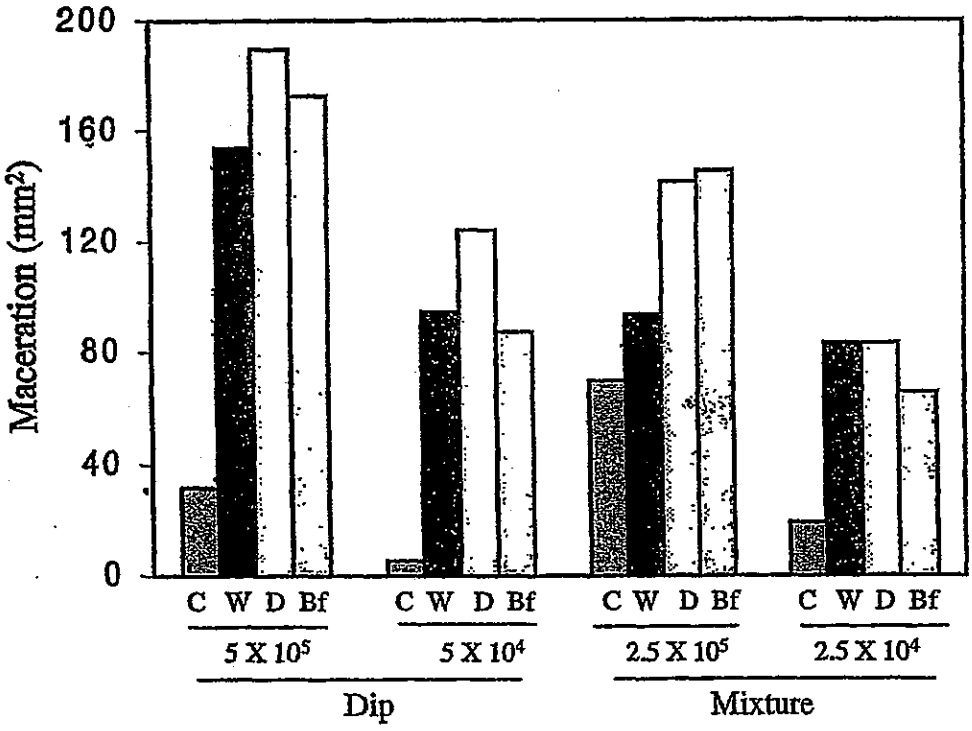

200
160
120
80
40
0
Maceration (mm²)
C W D Bf
C W D Bf
C W D Bf
C W D Bf
5 X 10⁵
5 X 10⁴
2.5 X 10⁵
2.5 X 10⁴
Dip
Mixture

Figure 13

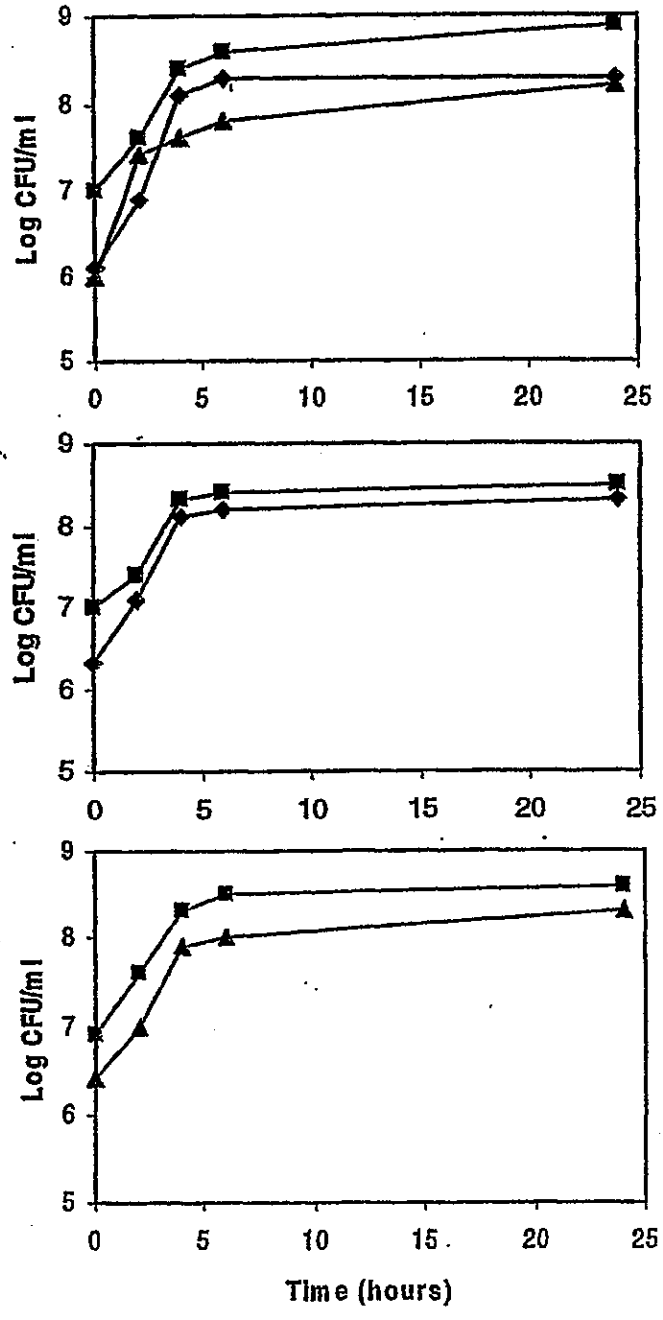
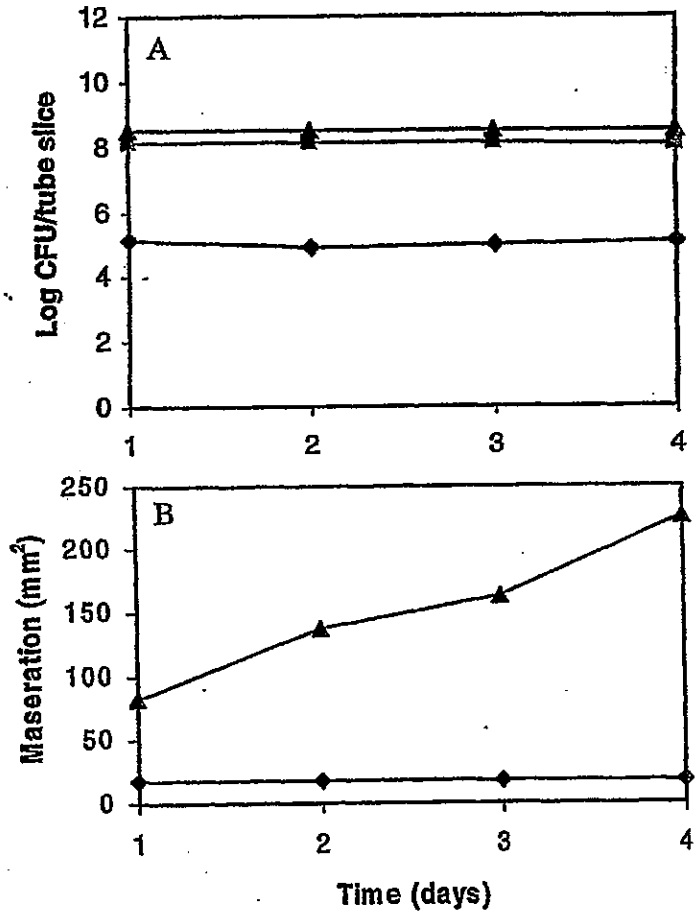

Log CFU/ml
9
8
7
6
5
0
5
10
15
20
25
Log CFU/ml
9
8
7
6
5
0
5
10
15
20
25
Log CFU/ml
9
8
7
6
5
0
5
10
15
20
25
Time (hours)

Figure 14


A
B
Log CFU/tube slice
Maseration (mm²)
Time (days)
0
2
4
6
8
10
12
50
100
150
200
250
1
2
3
4

SEQUENCE LISTING

<110> Institute of Molecular Agrobiology
Zhang, Lianhui
Dong, Yihu
Zhang, Haibao
Xu, Jinling

<120> Bacterial Strains, Genes and Enzymes for Control of Bacterial Diseases by Quenching
Quorum-Sensing Signals

<130> 2577-140

<160> 22

<170> PatentIn version 3.0

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cgccgcgacg tctgcgcgat gtcggcgtga cggacaacac gctcgccatg cttgcgtccg 180

acgcaatgaa acagagccgt ctgttggtca ataatccggt cgaagtccgc gaagaggatg 240

cgcttgcgct ctaccgcgag gcgttctgac ccatttctga cagcaatatc ttcagtccca 300

agggaggaaa acgagtgacc gatatcagac tttacatgct tcagtcgggt acgctgaaat 360

gcaaggtaca caacatcaag atgaaccagg ggaacggtgc agactatgag atccccgttc 420

cgtttttcct gattacccat ccgggcgggc acaccgtgat cgacggcggc aacgcgattg 480

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cgcttctcct gacgatcgat gctgcctaca ccctggacca ctgggaggag aaggctttgc 960

ctggcttcct cgcctcgacc gttgacacgg tccgttcggt tcagaaactc cgaacctatg 1020

ccgaaaagca tgatgcgacg gtcgttaccg gccatgaccc tgacgcgtgg gcgaacttca 1080

agaaggctcc cgaattttac gcgtaaataa aacgcgcaag tcaacagcca gatgcggcga 1140

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ccgtgtattt ctgcgcagag gccttttcag gatatacgcc ttcactcagg tcgttcgcgt 1260

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tactgtatta ctttatccca aactaaatgt aaaggtggat acataatgac agtaaagaag 180

ctttatttcg ttccagcagg tcgttgtatg ttagatcatt cttctgttaa tagtacaatc 240

gcgccgggaa atttattgaa cttacctgta tggtgttatc ttttggagac ggaagaaggt 300

cccattttag tagatacagg tatgccagaa agtgcggtta ataatgaaaa cttgtttgaa 360

gggacatttg cagaaggaca gattttaccg aaaatgactg aagaagatag aataatagct 420

attttaaaac gtgcagggta tgagccagat gacctcctat atattattag ttcacatttg 480

cattttgatc atgcaggagg aaatggtgct tttattaata ctccaatcat tatacagcgt 540

gctgaatatg aggcagcgca gtatagagag gaatatttga aagagtgtat actgccgaat 600

ttgaactaca aaattattga aggggattat gaagtggtac caggtgttca actattgtat 660

acaccaggac attcaccagg gcatcagtca ctattaattg agacagaaaa atctggtgtt 720

gtgttattaa ccattgatgc atcttatacg aaagagaatt ttgaagatga agtaccgttt 780

gctggatttg atccagaatt agctttatca tcaattaaac gtttaaaaga agttgtgatg 840

aaagagaagc cgcttgtttt ctttggacat gatatagagc aggaaaaggg atgtaaagtg 900

ttcccggaat atatatagtg caaaaagtca tgagcttacg tgctcatgac tttttgattt 960

aaataatttt tttaaataag ttataaactt ttttggaact atcttcattt aattgatagt 1020

acgtaagatt tacatcatca ggagtatctt gctgtgcaat catcacttcg ttactatgat 1080

gatcaactac ccatatgaaa tatttttttat aagtaccatc ctcaaatgta atccacatat 1140

cacaatctat taaatctgat ccttcttcat ctaatgttaa ttttcctttt ttggccgtat 1200

tcatactgtt aatgaatgtc tttaattcat ctgtttttgc gagaaagata tctttttttg 1260

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catttggatc cctttgagt 1339

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<213> Bacillus thuringiensis B1

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gagacggaag aaggtcctat tttagtagac acaggtatgc cagaaagtgc agttaataat 180

gaagggcttt ttaacggtac atttgttgaa ggacagatct taccgaaaat gactgaagaa 240

gatagaatcg tgaatatatt aaagcgtgtg gggtatgagc cggacgacct tttatatatt 300

attagttctc acttacattt tgatcatgca ggaggaaacg gtgcttttac aaatacacca 360

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tgtatattac cgcatttgaa ctacaaaatt attgaagggg attatgaagt ggtaccaggt 480

gttcaattat tgtatacgcc aggtcattct ccaggccatc agtcgctatt cattgagacg 540

gagcaatccg gttcagtttt attaatgatt gatgcatcgt acacgaaaga gaattttgaa 600

gatgaagtgc cgttcgcagg atttgatcca gaattagctt tatcttcaat taaacgttta 660

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gagacggaag aaggtcctat tttagtagac acaggtatgc cagaaagtgc agttaataat 180

gaagggcttt ttaacggtac atttgttgaa ggacagatct taccgaaaat gactgaagaa 240

gatagaatcg tgaatatatt aaagcgtgta gggtatgagc cggacgacct tttatatatt 300

attagttctc acttacattt tgatcatgca ggaggaaacg gtgcttttac aaatacacca 360

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tgtatattac cgcatttgaa ctacaaaatt attgaagggg attatgaagt ggtaccaggt 480

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gagcaatccg gttcagtttt attaacgatt gatgcatcgt acacgaaaga gaattttgaa 600

gatgaagtgc cgttcgcagg atttgatcca gaattagctt tatcttcaat taaacgttta 660

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aagagttgta gagtgttccc ggaatatata tag 753

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gaaaaatccg gtcttgtatt attaacgatt gatgcatctt atacgaaaga aaattttgaa 600

gatgaagtgc cgttcgcggg atttgattcg gaattagctt tatcttcaat taaacgttta 660

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gagacggaag aaggtcctat tttagtagac acaggtatgc cagaaagtgc agttaataat 180

gaagggcttt ttaacggtac atttgcaaaa ggacagattt taccgaaaat gactgaagaa 240

gatagaattg taactatttt aaaacgtgca gggtatgagc cagatgatct cctatatatt 300

attagttcgc acttgcattt tgatcatgca ggaggaaatg gtgctttttt gaatacgcca 360

atcattatac aacgtgctga atatgaggca gcgcagcata gagaggaata tttgaaagag 420

tgcatactac cagatttaaa ctacaaaatt attgaaggtg attatgaagt ggtacctggt 480

gttcggttat tgtatacacc aggacattct ccagggcatc agtcattatt aattgagacg 540

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gatgaagtac cgtttgcggg atttgattcg gaattagcct tatcttcaat taaacgttta 660

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aagggatgta aagtgttccc tgaatatata tag 753

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gagacagaag aagggcctat tttagtagat acaggtatgc cagaaagtgc agttaataat 180

gaagggcttt ttaacggtac atttgttgaa ggacagattt taccgaaaat gactgaagaa 240

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gagacagaag aggggcctat tttagtagat acaggtatgc cagaaagtgc agttaataat 180

gaagggcttt ttaacggtac atttgttgaa ggacagattt taccgaaaat gactgaagaa 240

gatagaatcg tgaatatatt aaagcgtgta gggtatgagc cggacgacct tttatatatt 300

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gacaattccg gttcagtttt attaacaatt gatgcatcgt acacgaaaga gaattttgaa 600

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<213> Bacillus thuringiensis B22

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<210> 10
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<213> Bacillus thuringiensis B25

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<212> PRT
<213> Agrobacterium tumefaciens M103

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Ile Pro Val Pro Phe Phe Leu Ile Thr His Pro Gly Gly His Thr Val
35 40 45

Ile Asp Gly Gly Asn Ala Ile Glu Val Ala Thr Asp Pro Arg Gly His
50 55 60

Trp Gly Gly Ile Cys Asp Val Tyr Trp Pro Val Leu Asp Lys Asp Gln
65 70 75 80

Gly Cys Val Asp Gln Ile Lys Ala Leu Gly Phe Asp Pro Ala Asp Val
85 90 95

Lys Tyr Val Val Gln Ser His Leu His Leu Asp His Thr Gly Ala Ile
100 105 110

Gly Arg Phe Pro Asn Ala Thr His Ile Val Gln Arg Ser Glu Tyr Glu
115 120 125

Tyr Ala Phe Thr Pro Asp Trp Phe Ala Gly Gly Gly Tyr Ile Arg Lys
130 135 140

Asp Phe Asp Lys Pro Gly Leu Lys Trp Gln Phe Leu Asn Gly Thr Gln
145 150 155 160

Asp Asp Tyr Tyr Asp Val Tyr Gly Asp Gly Thr Leu Thr Thr Ile Phe
165 170 175

Thr Pro Gly His Ala Pro Gly His Gln Ser Leu Leu Val Arg Leu Pro
180 185 190

Asn Ser Lys Pro Leu Leu Leu Thr Ile Asp Ala Ala Tyr Thr Leu Asp
195 200 205

His Trp Glu Glu Lys Ala Leu Pro Gly Phe Leu Ala Ser Thr Val Asp
210 215 220

Thr Val Arg Ser Val Gln Lys Leu Arg Thr Tyr Ala Glu Lys His Asp
225 230 235 240

Ala Thr Val Val Thr Gly His Asp Pro Asp Ala Trp Ala Asn Phe Lys
245 250 255

Lys Ala Pro Glu Phe Tyr Ala

260

<210> 12
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<400> 12

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20 25 30

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35 40 45

Val Asp Thr Gly Met Pro Glu Ser Ala Val Asn Asn Glu Asn Leu Phe
50 55 60

Glu Gly Thr Phe Ala Glu Gly Gln Ile Leu Pro Lys Met Thr Glu Glu
65 70 75 80

Asp Arg Ile Ile Ala Ile Leu Lys Arg Ala Gly Tyr Glu Pro Asp Asp
85 90 95

Leu Leu Tyr Ile Ile Ser Ser His Leu His Phe Asp His Ala Gly Gly
100 105 110

Asn Gly Ala Phe Ile Asn Thr Pro Ile Ile Ile Gln Arg Ala Glu Tyr
115 120 125

Glu Ala Ala Gln Tyr Arg Glu Glu Tyr Leu Lys Glu Cys Ile Leu Pro
130 135 140

Asn Leu Asn Tyr Lys Ile Ile Glu Gly Asp Tyr Glu Val Val Pro Gly
145 150 155 160

Val Gln Leu Leu Tyr Thr Pro Gly His Ser Pro Gly His Gln Ser Leu
165 170 175

Leu Ile Glu Thr Glu Lys Ser Gly Val Val Leu Leu Thr Ile Asp Ala
180 185 190

Ser Tyr Thr Lys Glu Asn Phe Glu Asp Glu Val Pro Phe Ala Gly Phe
195 200 205

Asp Pro Glu Leu Ala Leu Ser Ser Ile Lys Arg Leu Lys Glu Val Val
210 215 220

Met Lys Glu Lys Pro Leu Val Phe Phe Gly His Asp Ile Glu Gln Glu
225 230 235 240

Lys Gly Cys Lys Val Phe Pro Glu Tyr Ile
245 250

<210> 13

<211> 250
<212> PRT
<213> Bacillus thuringiensis B1

<400> 13

Met Thr Val Lys Lys Leu Tyr Phe Ile Pro Ala Gly Arg Cys Met Leu
1 5 10 15

Asp His Ser Ser Val Asn Ser Ala Leu Thr Pro Gly Lys Leu Leu Asn
20 25 30

Leu Pro Val Trp Cys Tyr Leu Leu Glu Thr Glu Glu Gly Pro Ile Leu
35 40 45

Val Asp Thr Gly Met Pro Glu Ser Ala Val Asn Asn Glu Gly Leu Phe
50 55 60

Asn Gly Thr Phe Val Glu Gly Gln Ile Leu Pro Lys Met Thr Glu Glu
65 70 75 80

Asp Arg Ile Val Asn Ile Leu Lys Arg Val Gly Tyr Glu Pro Asp Asp
85 90 95

Leu Leu Tyr Ile Ile Ser Ser His Leu His Phe Asp His Ala Gly Gly
100 105 110

Asn Gly Ala Phe Thr Asn Thr Pro Ile Ile Val Gln Arg Thr Glu Tyr
115 120 125

Glu Ala Ala Leu His Arg Glu Glu Tyr Met Lys Glu Cys Ile Leu Pro
130 135 140

His Leu Asn Tyr Lys Ile Ile Glu Gly Asp Tyr Glu Val Val Pro Gly
145 150 155 160

Val Gln Leu Leu Tyr Thr Pro Gly His Ser Pro Gly His Gln Ser Leu
165 170 175

Phe Ile Glu Thr Glu Gln Ser Gly Ser Val Leu Leu Met Ile Asp Ala
180 185 190

Ser Tyr Thr Lys Glu Asn Phe Glu Asp Glu Val Pro Phe Ala Gly Phe
195 200 205

Asp Pro Glu Leu Ala Leu Ser Ser Ile Lys Arg Leu Lys Glu Val Val
210 215 220

Lys Lys Glu Lys Pro Ile Ile Phe Phe Gly His Asp Thr Glu Gln Glu
225 230 235 240

Lys Ser Cys Arg Val Phe Pro Glu Tyr Ile
245 250

<210> 14
<211> 250
<212> PRT
<213> Bacillus thuringiensis B2

<400> 14

Met Thr Val Lys Lys Leu Tyr Phe Ile Pro Ala Gly Arg Cys Met Leu
1 5 10 15

Asp His Ser Ser Val Asn Ser Ala Leu Thr Pro Gly Lys Leu Leu Asn
20 25 30

Leu Pro Val Trp Cys Tyr Leu Leu Glu Thr Glu Glu Gly Pro Ile Leu
35 40 45

Val Asp Thr Gly Met Pro Glu Ser Ala Val Asn Asn Glu Gly Leu Phe
50 55 60

Asn Gly Thr Phe Val Glu Gly Gln Ile Leu Pro Lys Met Thr Glu Glu
65 70 75 80

Asp Arg Ile Val Asn Ile Leu Lys Arg Val Gly Tyr Glu Pro Asp Asp
85 90 95

Leu Leu Tyr Ile Ile Ser Ser His Leu His Phe Asp His Ala Gly Gly
100 105 110

Asn Gly Ala Phe Thr Asn Thr Pro Ile Ile Val Gln Arg Thr Glu Tyr
115 120 125

Glu Ala Ala Leu His Arg Glu Glu Tyr Met Lys Glu Cys Ile Leu Pro
130 135 140

His Leu Asn Tyr Lys Ile Ile Glu Gly Asp Tyr Glu Val Val Pro Gly
145 150 155 160

Val Gln Leu Leu Tyr Thr Pro Gly His Ser Pro Gly His Gln Ser Leu
165 170 175

Phe Ile Glu Thr Glu Gln Ser Gly Ser Val Leu Leu Thr Ile Asp Ala
180 185 190

Ser Tyr Thr Lys Glu Asn Phe Glu Asp Glu Val Pro Phe Ala Gly Phe
195 200 205

Asp Pro Glu Leu Ala Leu Ser Ser Ile Lys Arg Leu Lys Glu Val Val
210 215 220

Lys Lys Glu Lys Pro Ile Ile Phe Phe Gly His Asp Ile Glu Gln Glu
225 230 235 240

Lys Ser Cys Arg Val Phe Pro Glu Tyr Ile
245 250

<210> 15
<211> 250
<212> PRT
<213> Bacillus thuringiensis B17

<400> 15

Met Thr Val Lys Lys Leu Tyr Phe Val Pro Ala Gly Arg Cys Met Leu
1 5 10 15

Asp His Ser Ser Val Asn Ser Thr Leu Ala Pro Gly Asn Leu Leu Asn
20 25 30

Leu Pro Val Trp Cys Tyr Leu Leu Glu Thr Glu Glu Gly Pro Ile Leu
35 40 45

Val Asp Thr Gly Met Pro Glu Ser Ala Val Asn Asn Glu Gly Leu Phe
50 55 60

Asn Gly Thr Phe Val Glu Gly Gln Ile Leu Pro Lys Met Thr Glu Glu
65 70 75 80

Asp Arg Ile Val Asn Ile Leu Lys Arg Val Gly Tyr Glu Pro Asp Asp
85 90 95

Leu Leu Tyr Ile Ile Ser Ser His Leu His Phe Asp His Ala Gly Gly
100 105 110

Asn Gly Ala Phe Thr Asn Thr Pro Ile Ile Val Gln Arg Thr Glu Tyr
115 120 125

Glu Ala Ala Leu His Arg Glu Glu Tyr Met Lys Glu Cys Ile Leu Pro
130 135 140

His Leu Asn Tyr Lys Ile Ile Glu Gly Asp Tyr Glu Val Val Pro Gly
145 150 155 160

Val Gln Leu Leu Tyr Thr Pro Gly His Ser Pro Gly His Gln Ser Leu
165 170 175

Leu Ile Glu Thr Glu Lys Ser Gly Leu Val Leu Leu Thr Ile Asp Ala
180 185 190

Ser Tyr Thr Lys Glu Asn Phe Glu Asp Glu Val Pro Phe Ala Gly Phe
195 200 205

Asp Ser Glu Leu Ala Leu Ser Ser Ile Lys Arg Leu Lys Glu Val Val
210 215 220

Met Lys Glu Lys Pro Ile Ile Phe Phe Gly His Asp Ile Glu Gln Glu
225 230 235 240

Lys Gly Phe Lys Val Phe Pro Glu Tyr Ile
245 250

<210> 16
<211> 250
<212> PRT
<213> Bacillus thuringiensis B18

<400> 16

Met Thr Val Lys Lys Leu Tyr Phe Val Pro Ala Gly Arg Cys Met Leu
1 5 10 15

Asp His Ser Ser Val Asn Ser Ala Leu Thr Pro Gly Lys Leu Leu Asn
20 25 30

Leu Pro Val Trp Cys Tyr Leu Leu Glu Thr Glu Glu Gly Pro Ile Leu
35 40 45

Val Asp Thr Gly Met Pro Glu Ser Ala Val Asn Asn Glu Gly Leu Phe
50 55 60

Asn Gly Thr Phe Ala Lys Gly Gln Ile Leu Pro Lys Met Thr Glu Glu
65 70 75 80

Asp Arg Ile Val Thr Ile Leu Lys Arg Ala Gly Tyr Glu Pro Asp Asp
85 90 95

Leu Leu Tyr Ile Ile Ser Ser His Leu His Phe Asp His Ala Gly Gly
100 105 110

Asn Gly Ala Phe Leu Asn Thr Pro Ile Ile Ile Gln Arg Ala Glu Tyr
115 120 125

Glu Ala Ala Gln His Arg Glu Glu Tyr Leu Lys Glu Cys Ile Leu Pro
130 135 140

Asp Leu Asn Tyr Lys Ile Ile Glu Gly Asp Tyr Glu Val Val Pro Gly
145 150 155 160

Val Arg Leu Leu Tyr Thr Pro Gly His Ser Pro Gly His Gln Ser Leu
165 170 175

Leu Ile Glu Thr Glu Lys Ser Gly Pro Val Leu Leu Thr Ile Asp Ala
180 185 190

Ser Tyr Thr Lys Glu Asn Phe Glu Asp Glu Val Pro Phe Ala Gly Phe
195 200 205

Asp Ser Glu Leu Ala Leu Ser Ser Ile Lys Arg Leu Lys Glu Val Val
210 215 220

Met Lys Glu Lys Pro Ile Val Phe Phe Gly His Asp Ile Glu Gln Glu
225 230 235 240

Lys Gly Cys Lys Val Phe Pro Glu Tyr Ile
245 250

<210> 17
<211> 250
<212> PRT
<213> Bacillus thuringiensis B20

<400> 17

Met Thr Val Lys Lys Leu Tyr Phe Ile Pro Ala Gly Arg Cys Met Leu
1 5 10 15

Asp His Ser Ser Val Asn Ser Thr Leu Ala Pro Gly Asn Leu Leu Asn
20 25 30

Leu Pro Val Trp Cys Tyr Leu Leu Glu Thr Glu Glu Gly Pro Ile Leu
35 40 45

Val Asp Thr Gly Met Pro Glu Ser Ala Val Asn Asn Glu Gly Leu Phe
50 55 60

Asn Gly Thr Phe Val Glu Gly Gln Ile Leu Pro Lys Met Thr Glu Glu
65 70 75 80

Asp Arg Ile Val Asn Ile Leu Lys Arg Val Gly Tyr Glu Pro Asp Asp
85 90 95

Leu Leu Tyr Ile Ile Ser Ser His Leu His Phe Asp His Ala Gly Gly
100 105 110

Asn Gly Ala Phe Thr Asn Thr Pro Ile Ile Val Gln Arg Ala Glu Tyr
115 120 125

Glu Ala Ala Leu His Arg Glu Glu Tyr Met Lys Glu Cys Ile Leu Pro
130 135 140

His Leu Asn Tyr Lys Ile Ile Glu Gly Asp Tyr Glu Val Val Pro Gly
145 150 155 160

Val Gln Leu Leu Tyr Thr Pro Gly His Ser Pro Gly His Gln Ser Leu
165 170 175

Phe Ile Glu Thr Glu Gln Ser Gly Ser Val Leu Leu Thr Ile Asp Ala
180 185 190

Ser Tyr Thr Lys Glu Asn Phe Glu Asp Glu Val Pro Phe Ala Gly Phe
195 200 205

Asp Pro Glu Leu Ala Leu Ser Ser Ile Lys Arg Leu Lys Gly Val Val
210 215 220

Ala Glu Glu Lys Pro Ile Val Phe Phe Gly His Asp Ile Glu Gln Glu
225 230 235 240

Lys Gly Cys Arg Val Phe Pro Glu Tyr Ile
245 250

<210> 18
<211> 250
<212> PRT
<213> Bacillus thuringiensis B21

<400> 18

Met Thr Val Lys Lys Leu Tyr Phe Val Pro Ala Gly Arg Cys Met Leu
1 5 10 15

Asp His Ser Ser Val Asn Ser Thr Leu Ala Pro Gly Asn Leu Leu Asn
20 25 30

Leu Pro Val Trp Cys Tyr Leu Leu Glu Thr Glu Glu Gly Pro Ile Leu
35 40 45

Val Asp Thr Gly Met Pro Glu Ser Ala Val Asn Asn Glu Gly Leu Phe
50 55 60

Asn Gly Thr Phe Val Glu Gly Gln Ile Leu Pro Lys Met Thr Glu Glu
65 70 75 80

Asp Arg Ile Val Asn Ile Leu Lys Arg Val Gly Tyr Glu Pro Asp Asp
85 90 95

Leu Leu Tyr Ile Ile Ser Ser His Leu His Phe Asp His Ala Gly Gly
100 105 110

Asn Gly Ala Phe Thr Asn Thr Pro Ile Ile Val Gln Arg Ala Glu Tyr
115 120 125

Glu Ala Ala Leu His Arg Glu Glu Tyr Met Lys Glu Cys Ile Leu Pro
130 135 140

His Leu Asn Tyr Lys Ile Ile Glu Gly Asp Tyr Glu Val Val Pro Gly
145 150 155 160

Val Gln Leu Leu Tyr Thr Pro Gly His Ser Pro Gly His Gln Ser Leu
165 170 175

Phe Ile Glu Thr Asp Asn Ser Gly Ser Val Leu Leu Thr Ile Asp Ala
180 185 190

Ser Tyr Thr Lys Glu Asn Phe Glu Asp Glu Val Pro Phe Ala Gly Phe
195 200 205

Asp Pro Glu Leu Ala Leu Ser Ser Ile Lys Arg Leu Lys Gly Val Val
210 215 220

Ala Glu Glu Lys Pro Ile Val Phe Phe Gly His Asp Ile Glu Gln Glu
225 230 235 240

Lys Gly Cys Arg Val Phe Pro Glu Tyr Ile
245 250

<210> 19
<211> 250
<212> PRT
<213> Bacillus thuringiensis B22

<400> 19

Met Thr Val Lys Lys Leu Tyr Phe Ile Pro Ala Gly Arg Cys Met Leu
1 5 10 15

Asp His Ser Ser Val Asn Ser Thr Leu Ala Pro Gly Asn Leu Leu Asn
20 25 30

Leu Pro Val Trp Cys Tyr Leu Leu Glu Thr Glu Glu Gly Pro Ile Leu
35 40 45

Val Asp Thr Gly Met Pro Glu Ser Ala Val Asn Asn Glu Gly Leu Phe
50 55 60

Asn Gly Thr Phe Val Glu Gly Gln Ile Leu Pro Lys Met Thr Glu Glu
65 70 75 80

Asp Arg Ile Val Asn Ile Leu Lys Arg Val Gly Tyr Glu Pro Asp Asp
85 90 95

Leu Leu Tyr Ile Ile Ser Ser His Leu His Phe Asp His Ala Gly Gly
100 105 110

Asn Gly Ala Phe Thr Asn Thr Pro Ile Ile Val Gln Arg Ala Glu Tyr
115 120 125

Glu Ala Ala Leu His Arg Glu Glu Tyr Met Lys Glu Cys Ile Leu Pro
130 135 140

His Leu Asn Tyr Lys Ile Ile Glu Gly Asp Tyr Glu Val Val Pro Gly
145 150 155 160

Val Gln Leu Leu Tyr Thr Pro Gly His Ser Pro Gly His Gln Ser Leu
165 170 175

Phe Ile Glu Thr Glu Gln Ser Gly Ser Val Leu Leu Thr Ile Asp Ala
180 185 190

Ser Tyr Thr Lys Glu Asn Phe Glu Asp Glu Val Pro Phe Ala Gly Phe
195 200 205

Asp Pro Glu Leu Ala Leu Ser Ser Ile Lys Arg Leu Lys Gly Val Val
210 215 220

Ala Glu Glu Lys Pro Ile Val Phe Phe Gly His Asp Ile Glu Gln Glu
225 230 235 240

Lys Gly Cys Arg Val Phe Pro Glu Tyr Ile
245 250

<210> 20
<211> 250
<212> PRT
<213> Bacillus thuringiensis B25

<400> 20

Met Thr Val Lys Lys Leu Tyr Phe Ile Pro Ala Gly Arg Cys Met Leu
1 5 10 15

Asp His Ser Ser Val Asn Gly Thr Leu Ala Pro Gly Asn Leu Leu Asn
20 25 30

Leu Pro Val Trp Cys Tyr Leu Leu Glu Thr Glu Glu Gly Ala Ile Leu
35 40 45

Val Asp Thr Gly Met Pro Glu Ser Ala Val Asn Asn Glu Gly Leu Phe
50 55 60

Asn Gly Thr Phe Val Glu Gly Gln Ile Leu Pro Lys Met Thr Glu Glu
65 70 75 80

Asp Arg Ile Val Asn Ile Leu Lys Arg Val Gly Tyr Glu Pro Asp Asp
85 90 95

Leu Leu Tyr Ile Ile Ser Ser His Leu His Phe Asp His Ala Gly Gly
100 105 110

Asn Gly Ala Phe Thr Asn Thr Pro Ile Ile Val Gln Arg Thr Glu Tyr
115 120 125

Glu Ala Ala Leu His Arg Glu Glu Tyr Met Lys Glu Cys Ile Leu Pro
130 135 140

His Leu Asn Tyr Lys Ile Ile Glu Gly Asp Tyr Glu Val Val Pro Gly
145 150 155 160

Val Gln Leu Leu Tyr Thr Pro Gly His Ser Pro Gly His Gln Ser Leu
165 170 175

Phe Ile Glu Thr Glu Gln Ser Gly Ser Val Leu Leu Thr Ile Asp Ala
180 185 190

Ser Tyr Thr Lys Glu Asn Phe Glu Asp Glu Val Pro Phe Ala Gly Phe
195 200 205

Asp Pro Glu Leu Ala Leu Ser Ser Ile Lys Arg Leu Lys Gly Val Val
210 215 220

Ala Lys Glu Lys Pro Ile Val Phe Phe Gly His Asp Ile Glu Gln Glu
225 230 235 240

Lys Gly Cys Arg Val Phe Pro Glu Tyr Ile
245 250

<210> 21
<211> 256
<212> PRT
<213> Agrobacterium tumefaciens

<400> 21

Met Leu Gln Ser Gly Thr Leu Lys Cys Lys Val His Asn Ile Lys Met
1 5 10 15

Asn Gln Gly Asn Gly Ala Asp Tyr Glu Ile Pro Val Pro Phe Phe Leu
20 25 30

Ile Thr His Pro Ala Gly His Thr Val Ile Asp Gly Gly Asn Ala Ile
35 40 45

Glu Val Ala Thr Asp Pro Arg Gly His Trp Gly Gly Ile Cys Asp Val
50 55 60

Tyr Trp Pro Val Leu Asp Lys Asp Gln Gly Cys Val Asp Gln Ile Lys
65 70 75 80

Ala Leu Gly Phe Asp Pro Ala Asp Val Lys Tyr Val Val Gln Ser His
85 90 95

Leu His Leu Asp His Thr Gly Ala Ile Gly Arg Phe Pro Asn Ala Thr
100 105 110

His Ile Val Gln Arg Ser Glu Tyr Glu Tyr Ala Phe Thr Pro Asp Trp
115 120 125

Phe Ala Gly Gly Gly Tyr Ile Arg Lys Asp Phe Asp Lys Pro Gly Leu
130 135 140

Lys Trp Gln Phe Leu Asn Gly Ala Gln Asp Asp Tyr Tyr Asp Val Tyr
145 150 155 160

Gly Asp Gly Thr Leu Thr Thr Ile Phe Thr Pro Gly His Ala Pro Gly
165 170 175

His Gln Ser Phe Leu Val Arg Leu Pro Asn Ser Lys Pro Leu Leu Leu
180 185 190

Thr Ile Asp Ala Ala Tyr Thr Leu Asp His Trp Glu Glu Lys Ala Leu
195 200 205

Pro Gly Phe Leu Ala Ser Thr Val Asp Thr Val Arg Ser Val Gln Lys
210 215 220

Leu Arg Thr Tyr Ala Glu Lys His Asp Ala Thr Val Val Thr Gly His
225 230 235 240

Asp Pro Asp Ala Trp Ala Asn Phe Lys Lys Ala Pro Glu Phe Tyr Ala
245 250 255

<210> 22
<211> 248
<212> PRT
<213> Bacillus sp. 240B1

<400> 22

Met Thr Val Lys Lys Leu Tyr Phe Val Pro Ala Gly Arg Cys Met Leu
1 5 10 15

Asp His Ser Ser Val Asn Ser Thr Leu Thr Pro Gly Glu Leu Leu Asp
20 25 30

Leu Pro Val Trp Cys Tyr Leu Leu Glu Thr Glu Glu Gly Pro Ile Leu
35 40 45

Val Asp Thr Gly Met Pro Glu Ser Ala Val Asn Asn Glu Gly Leu Phe
50 55 60

Asn Gly Thr Phe Val Glu Gly Gln Val Leu Pro Lys Met Thr Glu Glu
65 70 75 80

Asp Arg Ile Val Asn Ile Leu Lys Arg Val Gly Tyr Glu Pro Glu Asp
85 90 95

Leu Leu Tyr Ile Ile Ser Ser His Leu His Phe Asp His Ala Gly Gly
100 105 110

Asn Gly Ala Phe Ile Asn Thr Pro Ile Ile Val Gln Arg Ala Glu Tyr
115 120 125

Glu Ala Ala Gln His Ser Glu Glu Tyr Leu Lys Glu Cys Ile Leu Pro
130 135 140

Asn Leu Asn Tyr Lys Ile Ile Glu Gly Asp Tyr Glu Val Val Pro Gly
145 150 155 160

Val Gln Leu Leu His Thr Pro Gly His Thr Pro Gly His Gln Ser Leu
165 170 175

Leu Ile Glu Thr Glu Lys Ser Gly Pro Val Leu Leu Thr Ile Asp Ala
180 185 190

Ser Tyr Thr Lys Glu Asn Phe Glu Asn Glu Val Pro Phe Ala Gly Phe
195 200 205

Asp Ser Glu Leu Ala Leu Ser Ser Ile Lys Arg Leu Lys Glu Val Val
210 215 220

Met Lys Glu Lys Pro Ile Val Phe Phe Gly His Asp Ile Glu Gln Glu
225 230 235 240

Arg Gly Cys Lys Val Phe Pro Glu
245